

06 May 2005

Alignment Results

Exhibit B

Alignment: Global Protein alignment against reference molecule
Parameters: Scoring matrix: BLOSUM 62

Reference molecule: SEQIDNO:6, Region 1-451

Number of sequences to align: 2

Settings: Similarity significance value cutoff: >= 60%



Summary of Percent Matches:

Reference:	SEQIDNO:6	1 - 451	(451 aa)	--
Sequence 2:	Kimura Tri101 Pro	1 - 451	(451 aa)	99%

SEQIDNO:6	1	mafkiqldtlgqlpgllsiytqisllypvsdssqyptivstfeqglkrfseavpwvagqv
Kimura Tri10	1	mafkiqldtlgqlpgllsiytqisllypvsdpsqyptivstfeqglkrfseavpwvagqv
SEQIDNO:6	61	kaegisegntgtsfiivpfedvprvvvkdldrddpsaptiegmrkagypmamfdeniapr
Kimura Tri10	61	kaegisegntgtsfiivpfedvprvvvkdldrddpsaptiegmrkagypmamfdeniapr
SEQIDNO:6	121	tlpigpgtgpdppkvillqlnfikggliltvngqhgamdmgvdavirllskacrndpf
Kimura Tri10	121	tlpigpgtgpdppkvillqlnfikggliltvngqhgamdmgvdavirllskacrndpf
SEQIDNO:6	181	teeemtamldrktiivpylenyitigpevdhqi vkadvaggdavltpvsaswafftfspka
Kimura Tri10	181	teeemtamldrktiivpylenyitigpevdhqi vkadvaggdavltpvsaswaffkfspka
SEQIDNO:6	241	mselkdaatktldastkfvstddalsafiwksasrvleridgsaptefcravdarpmg
Kimura Tri10	241	mselkdaatktldastkfvstddalsafiwksasrvleridgsaptefcravdarpmg
SEQIDNO:6	301	vsnnypgllqnmtyhnstigeianeslgatasrlrseldpasmrqrtrglatylhnnpdk
Kimura Tri10	301	vsnnypgllqnmtyhnstigeianeslgatasrlrseldpasmrqrtrglatylhnnpdk
SEQIDNO:6	361	snvsltadadpstsvmlsswakvgldwydfgfglgkpetvrrpifepveslmyfmpkkpd
Kimura Tri10	361	snvsltadadpstsvmlsswakvgldwydfgfglgkpetvrrpifepveslmyfmpkkpd
SEQIDNO:6	421	gefcaalslrddedmdrlkadkewtkyagyvg
Kimura Tri10	421	gefcaalslrddedmdrlkadkewtkyagyvg